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Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2008; month=9; day=12; hr=15; min=24; sec=40; ms=444; ]
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**Validated By CRFValidator v 1.0.3**

Application No: 10588114 Version No: 2.0

**Input Set:**

**Output Set:**

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**Finished:** 2008-08-14 10:59:29.870
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 686 ms
**Total Warnings:** 67
**Total Errors:** 0
**No. of SeqIDs Defined:** 99
**Actual SeqID Count:** 99

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| W | 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| W | 402 | Undefined organism found in <213> in SEQ ID (5) |
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| W | 213 | Artificial or Unknown found in <213> in SEQ ID (19) |
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| W | 213 | Artificial or Unknown found in <213> in SEQ ID (31) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (32) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (33) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (34) |

**Input Set:**

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**Started:** 2008-08-14 10:59:26.184
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**No. of SeqIDs Defined:** 99
**Actual SeqID Count:** 99

| Error code | Error Description |
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SEQUENCE LISTING

<110> OSTERMEIER, MARC A.
GUNTAS, GURKAN

<120> METHODS FOR MAKING AND USING MOLECULAR SWITCHES
INVOLVING CIRCULAR PERMUTATION

<130> 71699/62568

<140> 10588114
<141> 2008-08-14

<150> PCT/US05/002633
<151> 2005-01-28

<150> 60/628,997
<151> 2004-11-18

<150> 60/607,684
<151> 2004-09-07

<150> 60/557,152
<151> 2004-03-26

<150> 60/539,774
<151> 2004-01-28

<160> 99

<170> PatentIn Ver. 3.3

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20 25 30

Met Gly Leu Leu Thr
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<212> PRT
<213> Rous sarcoma virus

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<210> 4
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<212> PRT
<213> Unknown

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sequence

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Asp Ser Glu Glu Glu Leu Pro Thr Arg
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<213> Monkey virus SV40

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<210> 8
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<213> Unknown

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<210> 9
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<220>
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1 5

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<400> 11

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Tyr Gln Thr Ile
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<213> Homo sapiens

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1 5 10 15

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20 25 30

Glu Gln Phe
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<210> 13
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<212> PRT
<213> Saccharomyces cerevisiae

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20 25

<210> 14
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<213> Saccharomyces cerevisiae

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Thr Leu Cys Ser Ser Arg Tyr Leu Leu
20 25

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<213> Saccharomyces cerevisiae

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1 5 10 15

Ser Phe Tyr Ser Thr Ala Thr Gly Ala Ala Ser Lys Ser Gly Lys Leu
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Thr Gln Lys Leu Val Thr Ala Gly Val Ala Ala Ala Gly Ile Thr Ala
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Ser Thr Leu Leu Tyr Ala Asp Ser Leu Thr Ala Glu Ala Met Thr Ala
50 55 60

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<212> PRT
<213> Saccharomyces cerevisiae

<400> 16
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Ala Ala Thr Gly Thr Ala Ile Gly Ala Tyr Tyr Tyr Tyr Asn Gln Leu
20 25 30

Gln Gln Gln Gln Gln Arg Gly Lys Lys
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<210> 17
<211> 4
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<220>
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reticulum localizing sequence

<400> 17
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<211> 15
<212> PRT
<213> Human adenovirus type 19

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<210> 19
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<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Interleukin-2
sequence

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Val Thr Asn Ser
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<210> 20
<211> 29
<212> PRT
<213> Homo sapiens

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1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr
20 25

<210> 21
<211> 27
<212> PRT
<213> Homo sapiens

<400> 21
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1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn
20 25

<210> 22
<211> 18
<212> PRT
<213> Influenza A virus

<400> 22
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Gln Ile

<210> 23

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<212> PRT
<213> Unknown

<220>
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sequence

<400> 23
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Cys Ala Gly Asn Phe Val His Gly
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<210> 25
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<212> DNA
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<400> 25
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<210> 26
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<210> 27
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<212> DNA
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<223> a, c, g, t, unknown, or other

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<223> a, c, g, t, unknown, or other

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<210> 28
<211> 18
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<220>
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<210> 29
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<212> DNA
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<220>
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primer

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primer

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<210> 35
<211> 1995
<212> DNA
<213> Escherichia coli

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aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
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ctgttggctg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
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gtgatcaacg ccgccagcgg tcgtcagact gtcgatgaag ccctgaaaga cgcgcagact 1980
cgtatcacca agtaa 1995

<210> 36
<211> 664

<212> PRT
<213> Escherichia coli

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
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Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
             20                  25                  30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
         35                  40                  45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
     50                  55                  60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65                  70                  75                  80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
                 85                  90                  95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
            100                 105                 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
        115                 120                 125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
    130                 135                 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
145                 150                 155                 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
                165                 170                 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
            180                 185                 190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
        195                 200                 205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
    210                 215                 220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
225                 230                 235                 240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
                245                 250                 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
            260                 265                 270

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
        275                 280                 285

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Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
    290                 295                 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
305                 310                 315                 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
                325                 330                 335

Leu Ala Lys Asp Pro Arg Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp
            340                 345                 350

Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr
        355                 360                 365

Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met
    370                 375                 380

Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala
385                 390                 395                 400

Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg
                405                 410                 415

Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val
            420                 425                 430

Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg
        435                 440                 445

Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser
    450                 455                 460

His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
465                 470                 475                 480

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
                485                 490                 495

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
            500                 505                 510

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu
        515                 520                 525

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
    530                 535                 540

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
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